

Proposed Mechanism of the Antagonistic Relationship Between Terbinafine and a Novel Antifungal in Bakers Yeast

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Background

- Antibiotic resistant microbes were responsible for an estimated 4.95 million deaths in 2019 [1]
- 2-Hydroxyethylhydrazine (**HEH**) is a novel antifungal which enters the cell via an amine selective transporting protein encoded by the gene **HNM1**
- **HEH** achieves significant growth inhibition at lower concentrations than many currently used antifungals
- Combinatorial treatments can increase the effectiveness of treatment while lowering toxicity [2]

Terbinafine and HEH

When terbinafine and **HEH** are used in combination, a significant antagonistic relationship can be observed



between terbinafine and **HEH**

Methods: Nonessential Genetic Screening



Results

All Mutant "Hits" **Examples of** Affected Genes VMA8, VPH2 OPI1, VMA8, SIN4 All Gene Hits Random Gene Set OPI1, VPS15, PGD1 ---- Predicted Randor 0.5 OPI1, GAL11, False Positive Rate MED2 P-value: 3.5E-21 AOC: 0.8071

- The collected mutants were analyzed via a receiver operating characteristic curve, and gene ontology analysis
- Mutants were further categorized based on their sensitivity to **HEH**

Gene Function	P-va
Vacuolar Acidification	3.81 10
Biological Regulation	6.42 10
Regulation of RNA Biosynthesis	3.31 08
Response to Stimulus	5.37

Mutant "Hits": Phenotype A



		Well	SC	Terb.	HEH	Comb.
		A1	0.889	0.806	0.601	0.79
	OD Readings	A2	0.62	0.037	0.556	0.034
		A3	0.754	0.685	0.513	0.679
		A4	0.698	0.653	0.499	0.645
		A5	0.749	0.657	0.53	0.654
		A6	0.659	0.606	0.472	0.66

Mutant "Hits": Phenotype B





Proposed Mechanism



Future Directions

Continue to investigate the link between terbinafine and HNM1 Perform GC and TLC to analyze the lipid profile of yeast under our conditions

References:

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